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Asn Thr Pro Cys Ser Glu Asn Lys Leu Asp Ile Gln Glu Lys Lys Leu
130                      135                      140

Ile Asn Gln Glu Lys Lys Met Phe Arg Ile Arg Asn Arg Ser Tyr Ile
145                      150                      155                      160

Asp Arg Asp Ser Glu Tyr Leu Leu Gln Glu Asn Glu Pro Asp Gly Thr
165                      170                      175

Leu Asp Gln Lys Leu Leu Glu Asp Leu Gln Lys Lys Lys Asn Asp Leu
180                      185                      190

Arg Tyr Ile Glu Met Gln His Phe Arg Glu Lys Leu Pro Ser Tyr Gly
195                      200                      205

Met Gln Lys Glu Leu Val Asn Leu Ile Asp Asn His Gln Val Thr Val
210                      215                      220

Ile Ser Gly Glu Thr Gly Cys Gly Lys Thr Thr Gln Val Thr Gln Phe
225                      230                      235                      240

Ile Leu Asp Asn Tyr Ile Glu Arg Gly Lys Gly Ser Ala Cys Arg Ile
245                      250                      255

Val Cys Thr Gln Pro Arg Arg Ile Ser Ala Ile Ser Val Ala Glu Arg
260                      265                      270

Val Ala Ala Glu Arg Ala Glu Ser Cys Gly Ser Gly Asn Ser Thr Gly
275                      280                      285

Tyr Gln Ile Arg Leu Gln Ser Arg Leu Pro Arg Lys Gln Gly Ser Ile
290                      295                      300

Leu Tyr Cys Thr Thr Gly Ile Ile Leu Gln Trp Leu Gln Ser Asp Pro
305                      310                      315                      320

Tyr Leu Ser Ser Val Ser His Ile Val Leu Asp Glu Ile His Glu Arg
325                      330                      335

Asn Leu Gln Ser Asp Val Leu Met Thr Val Val Lys Asp Leu Leu Asn
340                      345                      350

Phe Arg Ser Asp Leu Lys Val Ile Leu Met Ser Ala Thr Leu Asn Ala
355                      360                      365

Glu Lys Phe Ser Glu Tyr Phe Gly Asn Cys Pro Met Ile His Ile Pro
370                      375                      380

Gly Phe Thr Phe Pro Val Val Glu Tyr Leu Leu Glu Asp Val Ile Glu
385                      390                      395                      400

Lys Ile Arg Tyr Val Pro Glu Gln Lys Glu His Arg Ser Gln Phe Lys
405                      410                      415

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(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 515 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Asn	Ile	Ser	Trp	Lys	Lys	Thr	Ile	Val	Thr	Arg	Phe	Leu	Lys	Leu	Val	1	5	10	15
Pro	Asp	Leu	Leu	Ala	Ile	Val	Gln	Arg	Lys	Lys	Lys	Glu	Gly	Glu	Glu	20	25	30	
Glu	Gln	Ala	Ile	Asn	Arg	Gln	Thr	Ala	Leu	Tyr	Thr	Leu	Lys	Leu	Leu	35	40	45	
Cys	Lys	Asn	Phe	Gly	Ala	Glu	Asn	Pro	Asp	Pro	Phe	Val	Pro	Val	Leu	50	55	60	
Ser	Thr	Ala	Val	Lys	Leu	Ile	Ala	Pro	Glu	Arg	Lys	Glu	Glu	Lys	Asn	65	70	75	80
Val	Leu	Gly	Ser	Ala	Leu	Leu	Cys	Met	Ala	Glu	Val	Thr	Ser	Thr	Leu	85	90	95	
Glu	Ala	Leu	Ala	Ile	Pro	Gln	Leu	Pro	Ser	Leu	Met	Pro	Ser	Leu	Leu	100	105	110	
Thr	Thr	Met	Lys	Asn	Thr	Ser	Glu	Leu	Val	Ser	Ser	Glu	Val	Tyr	Leu	115	120	125	
Leu	Ser	Ala	Leu	Ala	Ala	Leu	Gln	Lys	Val	Val	Glu	Thr	Leu	Pro	His	130	135	140	
Phe	Ile	Ser	Pro	Tyr	Leu	Glu	Gly	Ile	Leu	Ser	Gln	Val	Ile	His	Leu	145	150	155	160
Glu	Lys	Ile	Thr	Ser	Glu	Met	Gly	Ser	Ala	Ser	Gln	Ala	Asn	Ile	Arg	165	170	175	
Leu	Thr	Ser	Leu	Lys	Lys	Thr	Leu	Ala	Thr	Thr	Leu	Ala	Pro	Arg	Val	180	185	190	
Leu	Leu	Pro	Ala	Ile	Lys	Lys	Thr	Tyr	Lys	Gln	Ile	Glu	Lys	Asn	Trp	195	200	205	
Lys	Asn	His	Met	Gly	Pro	Phe	Met	Ser	Ile	Leu	Gln	Glu	His	Ile	Gly	210	215	220	
Ala	Met	Lys	Lys	Glu	Glu	Leu	Thr	Ser	His	Gln	Ser	Gln	Leu	Thr	Ala	225	230	235	240
Phe	Phe	Leu	Glu	Ala	Leu	Asp	Phe	Arg	Ala	Gln	His	Ser	Glu	Asn	Asp	245	250	255	
Leu	Glu	Glu	Val	Gly	Lys	Thr	Glu	Asn	Cys	Ile	Ile	Asp	Cys	Leu	Val	260	265	270	
Ala	Met	Val	Val	Lys	Leu	Ser	Glu	Val	Thr	Phe	Arg	Pro	Leu	Phe	Phe	275	280	285	
Lys	Leu	Phe	Asp	Trp	Ala	Lys	Thr	Glu	Asp	Ala	Pro	Lys	Asp	Arg	Leu	290	295	300	
Leu	Thr	Phe	Tyr	Asn	Leu	Ala	Asp	Cys	Ile	Ala	Glu	Lys	Leu	Lys	Gly	305	310	315	320
Leu	Phe	Thr	Leu	Phe	Ala	Gly	His	Leu	Val	Lys	Pro	Phe	Ala	Asp	Thr	325	330	335	

Leu Asp Gln Val Asn Ile Ser Lys Thr Asp Glu Ala Phe Phe Asp Ser
 340 345 350
 Glu Asn Asp Pro Glu Lys Cys Cys Leu Leu Leu Gln Phe Ile Leu Asn
 355 360 365
 Cys Leu Tyr Lys Ile Phe Leu Phe Asp Thr Gln His Phe Ile Ser Lys
 370 375 380
 Glu Arg Ala Gly Ala Leu Met Met Pro Leu Val Asp Gln Leu Glu Asn
 385 390 395 400
 Arg Leu Gly Gly Glu Glu Lys Phe Gln Glu Arg Val Thr Lys His Leu
 405 410 415
 Ile Pro Cys Ile Ala Gln Phe Ser Val Ala Met Ala Asp Asp Ser Leu
 420 425 430
 Trp Lys Pro Leu Asn Tyr Gln Ile Leu Leu Lys Thr Arg Asp Ser Ser
 435 440 445
 Pro Lys Val Arg Phe Ala Ala Leu Ile Thr Val Leu Ala Leu Ala Glu
 450 455 460
 Lys Leu Lys Glu Asn Tyr Ile Val Leu Leu Pro Glu Ser Ile Pro Phe
 465 470 475 480
 Leu Ala Glu Leu Met Glu Asp Glu Cys Glu Glu Val Glu His Gln Cys
 485 490 495
 Gln Lys Thr Ile Gln Gln Leu Glu Thr Val Leu Gly Glu Pro Leu Gln
 500 505 510
 Ser Tyr Phe
 515

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Gly Val Val Pro Asn Gly Arg Asp Ala Glu Ser Gly His Ser Leu Ala
 1 5 10 15
 Glu Gly Gln Ala Pro His Gly Leu Pro Gly Thr Pro Gly Ala Ser Gly
 20 25 30
 Gly Val Val Leu Gln Pro Arg Gly Arg Arg Arg Ala Asp Pro Pro His
 35 40 45
 Arg Gln Leu Arg Pro Glu Ala Phe Gly Asn His Arg Arg Ser Glu Phe
 50 55 60
 Leu Arg Leu Gln Val Glu Gly Gly Gly Cys Ser Gly Phe Gln Tyr Lys
 65 70 75 80
 Phe Ser Leu Asp Thr Val Ile Asn Pro Asp Asp Arg Val Phe Glu Gln
 85 90 95